

L Number	Hits	Search Text	DB	Time stamp
1	42	(hermeling-ronald\$ or hoffmann-james\$ or narasimhan-chak\$).in.	USPAT; US-PGPUB	2002/05/28 12:23
2	694	insulinotropin\$ or insulinotrophin\$ or glp or glpl or glucagon adj like adj (insulinotrop\$ or peptide or polypeptide)	USPAT; US-PGPUB	2002/05/28 12:31
3	8	((hermeling-ronald\$ or hoffmann-james\$ or narasimhan-chak\$).in.) and (insulinotropin\$ or insulinotrophin\$ or glp or glpl or glucagon adj like adj (insulinotrop\$ or peptide or polypeptide))	USPAT; US-PGPUB	2002/05/28 12:25
4	430942	crystal\$	USPAT; US-PGPUB	2002/05/28 12:36
5	6	((((hermeling-ronald\$ or hoffmann-james\$ or narasimhan-chak\$).in.) and (insulinotropin\$ or insulinotrophin\$ or glp or glpl or glucagon adj like adj (insulinotrop\$ or peptide or polypeptide))) and crystal\$	USPAT; US-PGPUB	2002/05/28 12:29
6	21	(insulinotropin\$ or insulinotrophin\$ or glp or glpl or glucagon adj like adj (insulinotrop\$ or peptide or polypeptide)) same crystal\$	USPAT; US-PGPUB	2002/05/28 12:38
7	19	((insulinotropin\$ or insulinotrophin\$ or glp or glpl or glucagon adj like adj (insulinotrop\$ or peptide or polypeptide)) same crystal\$) not (((hermeling-ronald\$ or hoffmann-james\$ or narasimhan-chak\$).in.) and (insulinotropin\$ or insulinotrophin\$ or glp or glpl or glucagon adj like adj (insulinotrop\$ or peptide or polypeptide))) and crystal\$)	USPAT; US-PGPUB	2002/05/28 12:33
8	61	(crystal\$).clm. and (530/308,324;514/12,21).ccls.	USPAT; US-PGPUB	2002/05/28 12:37
9	2	((insulinotropin\$ or insulinotrophin\$ or glp or glpl or glucagon adj like adj (insulinotrop\$ or peptide or polypeptide)) and ((crystal\$).clm. and (530/308,324;514/12,21).ccls.)) not (((hermeling-ronald\$ or hoffmann-james\$ or narasimhan-chak\$).in.) and (insulinotropin\$ or insulinotrophin\$ or glp or glpl or glucagon adj like adj (insulinotrop\$ or peptide or polypeptide))) and crystal\$)	USPAT; US-PGPUB	2002/05/28 12:37
10	10	(insulinotropin\$ or insulinotrophin\$ or glp or glpl or glucagon adj like adj (insulinotrop\$ or peptide or polypeptide)) and crystal\$	EPO; JPO; DERWENT	2002/05/28 12:50
11	1	2001-514598.NRAN.	DERWENT	2002/05/28 12:42
12	1	us-6284727-\$.did.	EPO; JPO; DERWENT	2002/05/28 12:50

Checked L4, L7, L9, L10, L12
JRK
5.28.2002

Set	Items	Description
S1	5686	INSULINOTROPIN? OR INSULINOTROPHIN? OR GLP OR GLP1 OR GLUC- AGON (W) LIKE (W) (PEPTIDE OR POLYPEPTIDE OR INSULINOTROP?)
S2	1272022	CRYSTAL?
S3	16	S1 AND S2
S4	5	S3 NOT (PY=2002 OR PY=2001 OR PY=2000 OR PY=1999 OR PC=US - OR PC=EP OR PC=WO)
S5	3	RD S4 (unique items)
?		

B 155, 5, 399

Checked SS

JRH

5.28.2002

CRFEP

Access DB# 63393

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Jeffery E. Russell Examiner #: 6222 Date: 3-28-2002
Art Unit: 1653 Phone Number 308 3977 Serial Number: 007997772
Mail Box and Bldg/Room Location: CM 119801 CM 119807 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need. MS

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Glucagon-Like Peptide 1 Crystals

Inventors (please provide full names): R. H. Herring, J. Jeffery E. Russell, J. H. Herring

Earliest Priority Filing Date: 12-11-1998

Far Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 1 in the Uniprot application sequence database (pending and issued) and in Genbank/EMBL/FASTA. Please require any hits to have 35 or fewer residues.

Thank you.
JHR

prot. 2

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher: <u>P. Schreiber</u>	NA Sequence (#) _____	STN _____	
Searcher Phone #: <u>308-4292</u>	AA Sequence (#) <u>1</u>	Dialog _____	
Searcher Location: <u>CM 16A03</u>	Structure (#) _____	Questel/Orbit _____	
Date Searcher Picked Up: <u>3/27</u>	Bibliographic _____	Dr.Link _____	
Date Completed: <u>4/2</u>	Litigation _____	Lexis/Nexis _____	
Searcher Prep & Review Time: <u>10</u>	Fulltext _____	Sequence Systems <u>1.000000</u>	
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____	
Online Time: <u>8</u>	Other _____	Other (specify) _____	

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 29, 2002, 10:05:32 ; Search time 23.75 Seconds
(without alignments)
96.685 Million cell updates/sec

Title: US-09-997-792-2
Perfect score: 138
Sequence: 1 XXEGTFTSDVSSYLXGQAAKXFIAWLVKGRX 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 253143

Minimum DB seq length: 0
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT.*
 22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score	Match					
1	131	94.9	28	17	AAR93056		N-terminally trunc
2	131	94.9	28	20	AAY39776		Glucagon like pept
3	131	94.9	28	20	AAY39777		Glucagon like pept
4	131	94.9	28	21	AAY67377		Inactivated glucag
5	131	94.9	28	22	AAB60251		Inactivated GLP-1
6	131	94.9	28	22	AAB36418		Glucagon-like pept
7	131	94.9	28	22	AAB36431		Glucagon-like pept
8	131	94.9	29	17	AAR93058		N-terminally trunc
9	131	94.9	29	21	AAY83146		Glucagon-like pept
10	131	94.9	29	21	AAY67376		Inactivated glucag
11	131	94.9	29	22	AAB60250		Inactivated GLP-1
12	131	94.9	29	22	AAB36417		Glucagon-like pept
13	131	94.9	29	22	AAB36430		Glucagon-like pept
14	131	94.9	30	15	AAR45435		Insulinotropin der
15	131	94.9	30	15	AAR63247		Insulinotropin (GL
16	131	94.9	30	16	AAR69063		Amidated Glucagon
17	131	94.9	30	16	AAR86787		Glucagon like pept
18	131	94.9	30	16	AAR79809		Glucagon like pept
19	131	94.9	30	16	AAR80548		Human glucagon lik
20	131	94.9	30	17	AAR98956		Target peptide (GL
21	131	94.9	30	17	AAR98975		GLP1(7-35)-NH2. S
22	131	94.9	30	17	AAR93060		N-terminally trunc
23	131	94.9	30	18	AAW16383		Glucagon-like pept
24	131	94.9	30	19	AAW29553		Met-8 GLP-1(7-36)-
25	131	94.9	30	19	AAW29555		Thr-8 GLP-1(7-36)-
26	131	94.9	30	19	AAW63288		Glucagon-like pept
27	131	94.9	30	19	AAW63182		GLP-1(7-36). Homo
28	131	94.9	30	19	AAW50903		Glucagon-like pept

29	131	94.9	30	19	AAW50906	Glucagon-like pept
30	131	94.9	30	20	AAAY42935	Glucagon-like pept
31	131	94.9	30	20	AAAY27374	Glucagon-like pept
32	131	94.9	30	20	AAAY39773	Glucagon like pept
33	131	94.9	30	20	AAAY34198	GLP-1 mutant pepti
34	131	94.9	30	20	AAAY31503	Glucagon-like pept
35	131	94.9	30	20	AAAY22168	GLP-1-like peptide
36	131	94.9	30	20	AAAY22166	GLP-1-like peptide
37	131	94.9	30	20	AAAY03719	Amino acid sequenc
38	131	94.9	30	21	AAB11283	GLP-1 peptide SEQ
39	131	94.9	30	21	AAB21335	GLP-1 analogue Val
40	131	94.9	30	21	AAB21336	GLP-1 analogue Thr
41	131	94.9	30	21	AAB21337	GLP-1 analogue Met
42	131	94.9	30	21	AAB21338	GLP-1 analogue Gly
43	131	94.9	30	21	AAB21340	GLP-1 peptide GLP-
44	131	94.9	30	21	AAB21351	GLP-1 analogue #11
45	131	94.9	30	21	AAB21352	GLP-1 analogue #12

ALIGNMENTS

RESULT 1

AAR93056

ID AAR93056 standard; peptide; 28 AA.

XX

AC AAR93056;

XX

DT 27-SEP-1996 (first entry)

XX

DE N-terminally truncated GLP-1 analog #12.

XX

KW Truncation; glucagon-like insulintropic peptide; GLP; proglucagon;

KW chemical synthesis; proteolysis; fragmentation; recombinant DNA; glucose;

KW stimulation; secretion; serum uptake; diabetes mellitus; hyperglycaemia.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 28

FT /note= "contains C-terminal NH2 group"

XX

PN EP699686-A2.

XX

PD 06-MAR-1996.

XX
PF 25-AUG-1995; 95EP-0305963.
XX
PR 30-AUG-1994; 94US-0297731.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Johnson WT, Yakubu-madus FE;
XX
DR WPI; 1996-130713/14.
XX
PT New C-terminal fragments of glucagon-like peptide GLP-1 - useful as
PT hypoglycaemic agents for treating diabetes
XX
PS Claim 2; Page 21; 23pp; English.
XX
CC Peptides AAR93045-60 represent examples of novel N-terminally truncated
CC glucagon-like insulinotropic peptide (GLP)-1 peptides. The peptides can
CC be synthesised chemically, derived by proteolytic fragmentation of
CC proglucagon or produced by recombinant DNA technology. This peptide
CC represents residues 9-36 of the full length GLP-1. The novel peptides
CC lack the insulinotropic activity of GLP-1 i.e. they do not stimulate
CC secretion of insulin, whilst retaining an activity allowing increased
CC serum uptake of glucose. The peptides are thus useful for treating
CC diabetes mellitus or hyperglycaemia.
XX
SQ Sequence 28 AA;

Query Match 94.9%; Score 131; DB 17; Length 28;
Best Local Similarity 92.9%; Pred. No. 1.1e-14;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EGTFTSDVSSYLXGQAAKXFIAWLVKGR 30
||||||| ||| |||||
Db 1 egtftsdvssylegqaakefiawlvkgr 28

RESULT 14
AAR45435
ID AAR45435 standard; protein; 30 AA.
XX
AC AAR45435;
XX

DT 27-JUN-1994 (first entry)
 XX
 DE Insulinotropin derivative.
 XX
 KW Insulinotropic; activity; enhancing insulin activity; treatment;
 KW Type II diabetes.
 XX
 OS Synthetic.
 XX
 PN WO9325579-A.
 XX
 PD 23-DEC-1993.
 XX
 PF 14-APR-1993; 93WO-US03388.
 XX
 PR 15-JUN-1992; 92US-0899073.
 XX
 PA (PFIZ) PFIZER INC.
 XX
 PI Andrews GC, Daumy GO, Francoeur ML, Larson ER;
 XX
 DR WPI; 1994-007457/01.
 XX
 PT New derivs. of glucagon-like peptide 1 and insulinotropin - used for
 PT enhancing insulin action in a mammal, partic. by iontophoretic admin.
 XX
 PS Claim 3; Page 20; 32pp; English.
 XX
 CC The sequence is that of a derivative of insulinotropin which
 CC has insulinotropic activity and is useful for enhancing insulin
 CC action in a mammal, partic. for treating Type II diabetes
 CC (claimed). It is partic. suited for delivery to a mammal by
 CC ionophoresis.
 XX
 SQ Sequence 30 AA;

Query Match 94.9%; Score 131; DB 15; Length 30;
 Best Local Similarity 92.9%; Pred. No. 1.1e-14;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EGTFTSDVSSYLXGQAAKXFIAWLVKGR 30

||||||| |||| |||||

Db 3 egtftsdvssylegqaakefiawlvkgr 30

Search completed: March 29, 2002, 10:10:55
Job time: 323 sec

OM protein - protein search, using sw model

Run on: March 29, 2002, 10:08:42 ; Search time 12.47 Seconds
(without alignments)
55.942 Million cell updates/sec

Title: US-09-997-792-2
Perfect score: 138
Sequence: 1 XXEGTFTSDVSSYLXGQAAKXFIAWLVKGRX 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 139820

Minimum DB seq length: 0
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	%					
Result		Query				
No.	Score	Match	Length	DB	ID	Description

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2	131	94.9	28	4	US-09-302-596-6	Sequence 6, Appli
3	131	94.9	28	5	PCT-US95-10793-9	Sequence 9, Appli
4	131	94.9	29	1	US-08-297-731-10	Sequence 10, Appl
5	131	94.9	29	1	US-08-297-731-11	Sequence 11, Appl
6	131	94.9	29	4	US-09-302-596-5	Sequence 5, Appli
7	131	94.9	29	5	PCT-US95-10793-10	Sequence 10, Appl
8	131	94.9	29	5	PCT-US95-10793-11	Sequence 11, Appl
9	131	94.9	30	1	US-08-066-480-6	Sequence 6, Appli
10	131	94.9	30	1	US-08-095-162-1	Sequence 1, Appli
11	131	94.9	30	1	US-08-297-731-12	Sequence 12, Appl
12	131	94.9	30	1	US-08-470-220A-1	Sequence 1, Appli
13	131	94.9	30	2	US-08-927-227-1	Sequence 1, Appli
14	131	94.9	30	3	US-08-967-374-1	Sequence 1, Appli
15	131	94.9	30	4	US-09-348-136-1	Sequence 1, Appli
16	131	94.9	30	4	US-08-961-405A-5	Sequence 5, Appli
17	131	94.9	30	4	US-08-915-918A-5	Sequence 5, Appli
18	131	94.9	30	4	US-09-302-596-4	Sequence 4, Appli
19	131	94.9	30	4	US-08-472-349-3	Sequence 3, Appli
20	131	94.9	30	5	PCT-US95-10793-12	Sequence 12, Appl
21	131	94.9	30	5	PCT-US95-15800-27	Sequence 27, Appl
22	131	94.9	31	1	US-09-025-951-1	Sequence 1, Appli
23	131	94.9	31	1	US-08-095-162-3	Sequence 3, Appli
24	131	94.9	31	1	US-08-295-913A-1	Sequence 1, Appli
25	131	94.9	31	1	US-08-470-220A-3	Sequence 3, Appli
26	131	94.9	31	2	US-09-047-663-1	Sequence 1, Appli
27	131	94.9	31	2	US-09-047-663-2	Sequence 2, Appli
28	131	94.9	31	2	US-08-807-263-3	Sequence 3, Appli
29	131	94.9	31	3	US-08-967-374-3	Sequence 3, Appli
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31	131	94.9	31	4	US-08-961-405A-2	Sequence 2, Appli
32	131	94.9	31	4	US-08-961-405A-6	Sequence 6, Appli
33	131	94.9	31	4	US-08-915-918A-1	Sequence 1, Appli
34	131	94.9	31	4	US-08-915-918A-2	Sequence 2, Appli
35	131	94.9	31	4	US-09-302-596-3	Sequence 3, Appli
36	131	94.9	31	4	US-08-472-349-2	Sequence 2, Appli
37	131	94.9	31	5	PCT-US95-15800-28	Sequence 28, Appl
38	128	92.8	28	1	US-08-297-731-13	Sequence 13, Appl
39	128	92.8	28	5	PCT-US95-10793-13	Sequence 13, Appl
40	128	92.8	31	2	US-08-835-231-12	Sequence 12, Appl
41	128	92.8	31	4	US-09-258-750-1	Sequence 1, Appli
42	128	92.8	31	4	US-09-258-750-2	Sequence 2, Appli
43	128	92.8	31	4	US-09-258-750-3	Sequence 3, Appli
44	128	92.8	31	4	US-09-258-750-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-08-297-731-9

; Sequence 9, Application US/08297731

; Patent No. 5574008

; GENERAL INFORMATION:

; APPLICANT: Johnson, William T.

; APPLICANT: Yakubu-Madus, Fatima E.

; TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENTS OF

; TITLE OF INVENTION: GLUCAGON-LIKE INSULINOTROPIC PEPTIDE

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Eli Lilly and Company/RSM

; STREET: Lilly Corporate Center

; CITY: Indianapolis

; STATE: IN

; COUNTRY: USA

; ZIP: 46285

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/297,731

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Maciak, Ronald S.

; REGISTRATION NUMBER: 35,262

; REFERENCE/DOCKET NUMBER: X9630

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317-276-1664

; TELEFAX: 317-277-1917

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 27..28
; OTHER INFORMATION: /note= "C-terminal amide"
US-08-297-731-9

Query Match 94.9%; Score 131; DB 1; Length 28;
Best Local Similarity 92.9%; Pred. No. 1.8e-14;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EGTFTSDVSSYLXGQAAKXFIAWLVKGR 30
||||||| ||| |||||
Db 1 EGTFTSDVSSYLEGQAAKEFIAWLVKGR 28

Search completed: March 29, 2002, 10:11:14
Job time: 152 sec

Search completed: March 29, 2002, 10:13:13

Job time: 186 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 29, 2002, 10:09:22 ; Search time 12.79 Seconds
(without alignments)
184.629 Million cell updates/sec

Title: US-09-997-792-2
Perfect score: 138
Sequence: 1 XXEGTFTSDVSSYLXGQAAKXFIAWLVKGRX 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 7547

Minimum DB seq length: 0
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%	No.	Score	Match	Length	DB	ID	Description
1	105	76.1	30	2	B61125				glucagon-like pept

2	105	76.1	30	2	C61125	glucagon-like pept
3	93	67.4	30	2	S44473	glucagon-like pept
4	82	59.4	29	2	S07211	glucagon - marbled
5	80	58.0	29	1	GCDF	glucagon - smaller
6	78	56.5	29	1	GCEN	glucagon - elephan
7	75	54.3	29	1	GCOPV	glucagon - North A
8	75	54.3	29	2	A91740	glucagon - turkey
9	75	54.3	29	2	A91741	glucagon - rabbit
10	75	54.3	29	2	A91742	glucagon - Arabian
11	75	54.3	29	2	C39258	glucagon - common
12	75	54.3	31	2	S44472	glucagon G2 - Nort
13	73	52.9	29	1	GCDK	glucagon - duck
14	73	52.9	29	1	A61583	glucagon - ostrich
15	73	52.9	29	1	GCTTS	glucagon - slider
16	73	52.9	31	2	S44471	glucagon G1 - Nort
17	70	50.7	29	2	C60840	glucagon I - Europ
18	69	50.0	29	1	GCCB	glucagon - Chinchi
19	68	49.3	29	1	GCFLE	glucagon - Europea
20	68	49.3	29	2	A61135	glucagon - bigeye
21	68	49.3	29	2	S39018	glucagon - bowfin
22	49.5	35.9	31	2	S39019	glucagon-like pept
23	46	33.3	17	2	A60317	glucagon-like pept
24	40	29.0	27	1	S07443	secretin - human
25	39	28.3	27	2	A61071	pituitary adenylat
26	35.5	25.7	30	2	B53088	factor IX/factor X
27	35	25.4	26	1	B57082	secretin - guinea
28	35	25.4	27	1	SEBO	secretin - bovine
29	35	25.4	27	1	SESH	secretin - sheep
30	35	25.4	27	2	A27267	secretin - dog
31	32.5	23.6	31	2	S74160	18K protein - shee
32	32	23.2	27	2	T36655	probable small mem
33	31	22.5	25	2	JQ0361	vasoactive intesti
34	31	22.5	27	1	SECH	secretin - chicken
35	29	21.0	27	2	C60415	secretin - rabbit
36	29	21.0	27	4	S53133	probable pre-core
37	29	21.0	27	4	S53168	probable pre-core
38	29	21.0	27	4	S53154	probable pre-core
39	29	21.0	27	4	S53259	probable pre-core
40	29	21.0	27	4	S20754	probable pre-core
41	29	21.0	30	2	S07065	rRNA N-glycosidase
42	29	21.0	35	1	HWGHD	exendin-2 - Gila m
43	28	20.3	27	4	S53139	probable pre-core
44	28	20.3	27	4	S53151	probable pre-core
45	28	20.3	27	4	S53213	probable pre-core

ALIGNMENTS

RESULT 1

B61125

glucagon-like peptide - American eel

C;Species: *Anguilla rostrata* (American eel)

C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Nov-1997

C;Accession: B61125

R;Conlon, J.M.; Andrews, P.C.; Thim, L.; Moon, T.W.

Gen. Comp. Endocrinol. 82, 23-32, 1991

A;Title: The primary structure of glucagon-like peptide but not insulin has been conserved between the American eel, *Anguilla rostrata* and the European eel, *Anguilla anguilla*.

A;Reference number: A61125; MUID:91340068

A;Accession: B61125

A;Molecule type: protein

A;Residues: 1-30 <CON>

C;Superfamily: glucagon

C;Keywords: amidated carboxyl end; duplication

F;1-30/Product: glucagon-like peptide #status experimental <GLP>

F;30/Modified site: amidated carboxyl end (Arg) #status predicted

Query Match 76.1%; Score 105; DB 2; Length 30;

Best Local Similarity 71.4%; Pred. No. 6.3e-10;

Matches 20; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 EGTFTSDVSSYLXGQAAKXFIWLKGR 30

|||:||||| ||| |:| ||

Db 3 EGTYTSDVSSYLQDQAAKEFVSWLKTGR 30

Search completed: March 29, 2002, 10:11:33

Job time: 131 sec

OM protein - protein search, using sw model

Run on: March 29, 2002, 10:11:17 ; Search time 10.06 Seconds
(without alignments)
112.983 Million cell updates/sec

Title: US-09-997-792-2

Perfect score: 138

Sequence: 1 XXEGTFTSDVSSYLXGQAAKXFIAWLVKGRX 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 2214

Minimum DB seq length: 0
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB ID	Description
	Score					
1	105	76.1	30	1	GLUM_ANGAN	P41521 anguilla an
2	100	72.5	33	1	GLU2_ORENI	P81027 oreochromis
3	82	59.4	29	1	GLUC_TORMA	P09567 torpedo mar
4	80	58.0	29	1	GLUC_SCYCA	P09687 scyliorhinu
5	78	56.5	29	1	GLUC_CALMI	P13189 callorhynch

6	75	54.3	29	1	GLUC_DIDMA	P18108 didelphis m
7	75	54.3	29	1	GLUC_LAMFL	Q9prq9 lampetra fl
8	75	54.3	29	1	GLUC_RABIT	P25449 oryctolagus
9	73	52.9	29	1	GLUC_ANAPL	P01276 anas platyr
10	69	50.0	29	1	GLUC_CHIBR	P31297 chinchilla
11	68	49.3	29	1	GLUC_PLAFE	P23062 platichthys
12	35	25.4	27	1	SECR_CANFA	P09910 canis famil
13	35	25.4	27	1	SECR_SHEEP	P31299 ovis aries
14	31	22.5	25	1	VIP_GADMO	P09684 gadus morhu
15	31	22.5	27	1	SECR_CHICK	P01280 gallus gall
16	31	22.5	35	1	EXE2_HEL SU	P04204 heloderma s
17	29	21.0	27	1	SECR_RABIT	P32647 oryctolagus
18	29	21.0	30	1	RIPS_MOMCO	P20655 momordica c
19	28	20.3	24	1	IR31_HAEIN	P35756 haemophilus
20	28	20.3	35	1	TX1_GRASP	P56852 grammostola
21	27	19.6	28	1	VIP_ALLMI	P48142 alligator m
22	27	19.6	28	1	VIP_RANRI	P81016 rana ridibu
23	27	19.6	32	1	Y169_TREPA	O83199 treponema p
24	27	19.6	34	1	TX1_SCOGR	P56855 scodra gris
25	26	18.8	26	1	DMS5_PHYBI	P81487 phyllomedus
26	25	18.1	28	1	VIP_SCYCA	P09685 scylorhinu
27	25	18.1	31	1	CU54_LOCM I	P11738 locusta mig
28	25	18.1	31	1	GP37_BPSP1	O48393 bacterioph a
29	25	18.1	35	1	TX2_GRASP	P56853 grammostola
30	24	17.4	28	1	LPL_SALTY	P03062 salmonella
31	24	17.4	30	1	PSAM_PINTH	P41601 pinus thunb
32	24	17.4	33	1	GAE2_RANRU	P80396 rana rugosa
33	24	17.4	33	1	GAE3_RANRU	P80397 rana rugosa
34	24	17.4	35	1	YRKM_BACSU	P54440 bacillus su
35	23	16.7	19	1	ALL7_OLEEU	P81430 olea europa
36	23	16.7	31	1	DIUX_DIPPU	P82372 diploptera
37	23	16.7	33	1	STC_ONCMY	P43648 oncorhynch u
38	23	16.7	33	1	YJX_SALTY	P39432 salmonella
39	23	16.7	35	1	END4_YEREN	P42691 yersinia en
40	22	15.9	13	1	TEML_RANTE	P57104 rana tempor
41	22	15.9	14	1	MAST_VESBA	P21654 vespa basal
42	22	15.9	28	1	GTS5_CHICK	P20137 gallus gall
43	22	15.9	31	1	LCCB_LEUME	P81052 leuconostoc
44	22	15.9	32	1	RIP2_PHYDI	P34967 phytolacca
45	22	15.9	33	1	GAST_DIDMA	P33713 didelphis m

ALIGNMENTS

RESULT 1
 GLUM_ANGAN
 ID GLUM_ANGAN STANDARD; PRT; 30 AA.
 AC P41521;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE GLUCAGON-LIKE PEPTIDE (GLP).
 OS *Anguilla anguilla* (European freshwater eel), and
 OS *Anguilla rostrata* (American eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguilloidei;
 OC Anguillidae; *Anguilla*.
 OX NCBI_TaxID=7936, 7938;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=91340068; PubMed=1874385;
 RA Conlon J.M., Andrews P.C., Thim L., Moon T.W.;
 RT "The primary structure of glucagon-like peptide but not insulin has
 RT been conserved between the American eel, *Anguilla rostrata* and the
 RT European eel, *Anguilla anguilla*.";
 RL Gen. Comp. Endocrinol. 82:23-32(1991).
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; B61125; B61125.
 DR PIR; C61125; C61125.
 DR HSSP; P01274; 1GCN.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation.
 FT MOD_RES 30 30 AMIDATION.
 SQ SEQUENCE 30 AA; 3376 MW; 592DA5EABD6E49D0 CRC64;

Query Match 76.1%; Score 105; DB 1; Length 30;
 Best Local Similarity 71.4%; Pred. No. 2.1e-10;
 Matches 20; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 EGTFTSDVSSYLXGQAAKXFIAWLVKGR 30
 |||:||||| ||| |:| ||
 Db 3 EGTYTSDVSSYLQDQAAKEFVSWLKTGR 30

Search completed: March 29, 2002, 10:14:20
Job time: 183 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 29, 2002, 10:10:57 ; Search time 21.96 Seconds
(without alignments)
206.486 Million cell updates/sec

Title: US-09-997-792-2
Perfect score: 138
Sequence: 1 XXEGTFTSDVSSYLXGQAAKXFIAWLVKGRX 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 16942

Minimum DB seq length: 0
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					Description
	No.	Score	Match	Length	DB ID	
1	37	26.8	35	2	Q9R4M5	Q9r4m5 amycolatops
2	35.5	25.7	30	13	Q9PS05	Q9ps05 bothrops ja
3	35	25.4	28	13	Q9PRN8	Q9prn8 carassius a
4	33	23.9	33	6	Q9TSD2	Q9tsd2 bos taurus
5	32	23.2	25	4	Q9UNK3	Q9unk3 homo sapien
6	32	23.2	26	4	Q9UQN6	Q9uqn6 homo sapien
7	32	23.2	27	2	Q9X902	Q9x902 streptomyce
8	31	22.5	29	12	Q86242	Q86242 human rotav
9	31	22.5	29	12	Q86243	Q86243 human rotav
10	30	21.7	25	12	O37187	O37187 hepatitis c
11	30	21.7	25	12	O37188	O37188 hepatitis c
12	30	21.7	25	12	O37189	O37189 hepatitis c
13	30	21.7	25	12	O37190	O37190 hepatitis c
14	30	21.7	25	12	O37191	O37191 hepatitis c
15	30	21.7	25	12	O37192	O37192 hepatitis c
16	30	21.7	25	12	O37193	O37193 hepatitis c
17	30	21.7	25	12	O37194	O37194 hepatitis c
18	30	21.7	35	2	P82554	P82554 streptococc
19	29	21.0	20	2	Q9R5A6	Q9r5a6 thiobacillu
20	29	21.0	25	12	Q67095	Q67095 influenza a
21	29	21.0	27	12	Q68059	Q68059 hepatitis b
22	29	21.0	27	12	Q67958	Q67958 hepatitis b
23	29	21.0	27	12	Q67975	Q67975 hepatitis b
24	29	21.0	27	12	Q67988	Q67988 hepatitis b
25	29	21.0	27	12	Q81171	Q81171 hepatitis b
26	29	21.0	27	12	Q9WRL1	Q9wrl1 hepatitis b
27	29	21.0	27	12	Q89528	Q89528 hepatitis b
28	29	21.0	29	6	Q9N1W3	Q9n1w3 equus cabal
29	29	21.0	29	12	Q81170	Q81170 hepatitis b
30	29	21.0	30	12	Q81176	Q81176 hepatitis b
31	29	21.0	31	12	Q81188	Q81188 hepatitis b
32	29	21.0	33	2	Q53421	Q53421 xanthobacte
33	28	20.3	27	12	Q67945	Q67945 hepatitis b
34	28	20.3	27	12	Q67963	Q67963 hepatitis b
35	28	20.3	27	12	Q67972	Q67972 hepatitis b
36	28	20.3	27	12	Q68022	Q68022 hepatitis b

37	28	20.3	27	12	O37181	O37181 hepatitis c
38	28	20.3	27	12	O37197	O37197 hepatitis c
39	28	20.3	27	12	O37216	O37216 hepatitis c
40	28	20.3	28	2	P97144	P97144 staphylococ
41	28	20.3	28	4	Q16325	Q16325 homo sapien
42	28	20.3	29	12	Q86241	Q86241 human rotav
43	28	20.3	29	12	Q86240	Q86240 human rotav
44	28	20.3	29	12	Q86244	Q86244 human rotav
45	28	20.3	29	12	Q86245	Q86245 human rotav

ALIGNMENTS

RESULT 1

Q9R4M5

ID Q9R4M5 PRELIMINARY; PRT; 35 AA.

AC Q9R4M5;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE PREPHENATE DEHYDRATASE (FRAGMENT).

OS Amycolatopsis methanolica.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.

OX NCBI_TaxID=1814;

RN [1]

RP SEQUENCE.

RX MEDLINE=95275250; PubMed=7755580;

RA Euverink G.J., Wolters D.J., Dijkhuizen L.;

RT "Prephenate dehydratase of the actinomycete Amycolatopsis methanolica:

RT purification and characterization of wild-type and deregulated mutant

RT proteins.";

RL Biochem. J. 308:313-320(1995).

SQ SEQUENCE 35 AA; 3646 MW; 3AA0FC5D5F97887F CRC64;

Query Match 26.8%; Score 37; DB 2; Length 35;

Best Local Similarity 42.9%; Pred. No. 59;

Matches 9; Conservative 3; Mismatches 1; Indels 8; Gaps 1;

Qy 4 GTFTSDVSSYLXGQAAKXFIA 24

|||| |:::|:

Db 10 GTFT-----GEAARTFMA 22

Search completed: March 29, 2002, 10:14:04

Job time: 187 sec